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SEP 08



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1600

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/524,101D

DATE: 08/29/2003

TIME: 14:18:55

Input Set : A:\EX00-015C afterfinalpatentin.txt

Output Set : N:\CRF4\08292003\I524101D.raw

3 <110> APPLICANT: EXELIXIS, INC.  
 5 <120> TITLE OF INVENTION: INSECT P53 TUMOR SUPPRESSOR GENES AND PROTEINS  
 7 <130> FILE REFERENCE: EX00015C FIRST AMENDMENT  
 9 <140> CURRENT APPLICATION NUMBER: US 09/524,101D  
 10 <141> CURRENT FILING DATE: 2000-03-13  
 12 <150> PRIOR APPLICATION NUMBER: US 09/268,969  
 13 <151> PRIOR FILING DATE: 1999-03-16  
 15 <150> PRIOR APPLICATION NUMBER: US 60/184,373  
 16 <151> PRIOR FILING DATE: 2000-02-23  
 18 <160> NUMBER OF SEQ ID NOS: 35  
 20 <170> SOFTWARE: PatentIn version 3.2  
 22 <210> SEQ ID NO: 1  
 23 <211> LENGTH: 1573  
 24 <212> TYPE: DNA  
 25 <213> ORGANISM: Drosophila melanogaster  
 27 <400> SEQUENCE: 1

P.6

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30	atttagcctc	cttccccaac	aagatcgctt	gatcagatat	agccgactaa	gatgtatata	120
32	tcacagccaa	tgtcgtggca	caaagaaagc	actgattccg	aggatgactc	cacggaggtc	180
34	gatataaagg	aggatattcc	gaaaacggtg	gaggtatcgg	gatcggaatt	gaccacggaa	240
36	cccatggcct	tcttgcaagg	attaaactcc	gggaatctga	tgcagttcag	ccagcaatcc	300
38	gtgctgcgcg	aaatgatgct	gcaggacatt	cagatccagg	cgaacacgct	gccccagcta	360
40	gagaatcaca	acatcggtgg	ttattgcttc	agcatggttc	tggatgagcc	gccccagtct	420
42	ctttggatgt	actcgattcc	gctgaacaag	ctctacatcc	ggatgaacaa	ggccttcaac	480
44	gtggacgttc	agttcaagtc	taaaatgcc	atccaaccac	ttaatttgcg	tgtgttcctt	540
46	tgtttctcca	atgatgtgag	tgtctccgtg	gtccgctgtc	aaaatcacct	tagcgttgag	600
48	cctttgacgg	ccaataacgc	aaaaatgcgc	gagagcttgc	tgcgcagcga	gaatcccaac	660
50	agtgtatatt	gtggaaatgc	tcagggcaag	ggaatttccg	agcgtttttc	cgttgtagtc	720
52	cccctgaaca	tgagccggtc	tgtaaccgcg	agtgggctca	cgcgccagac	cctggccttc	780
54	aagttcgtct	gccaaaactc	gtgtatcggg	cgaaaagaaa	cttccttagt	cttctgcctg	840
56	gagaaagcat	gcggcgatat	cgtgggacag	catgttatac	atgttaaaat	atgtacgtgc	900
58	cccaagcggg	atcgcatcca	agacgaacgc	cagctcaata	gcaagaagcg	caagtccgtg	960
60	ccggaagccg	ccgaagaaga	tgagccgtcc	aaggtgcgtc	ggtgcattgc	tataaagacg	1020
62	gaggacacgg	agagcaatga	tagccgagac	tgcgacgact	ccgccgcaga	gtggaacgtg	1080
64	tgcggaacac	cggatggcga	ttaccgtctg	gctattacgt	gccccataaa	ggaatggctg	1140
66	ctgcagagca	tgcaggggcat	gattaaggag	gcggcggtcg	aagtccctgcg	caatcccaac	1200
68	caagagaatc	tacgtcgcca	tgccaacaaa	ttgctgagcc	ttaagaaacg	tgccctacgag	1260
70	ctgccatgac	ttctgatctg	gtcgacaatc	tcccaggtat	cagatacctt	tgaaatgtgt	1320
72	tgcattctgtg	gggtatacta	catagctatt	agtatcttaa	gtttgtatta	gtccttgctt	1380
74	gtaaggcggt	taacggtgat	attccccctt	tggcatgttc	gatggccgaa	aagaaaacat	1440
76	ttttatattt	ttgatagtat	actggtgtta	actgcagttc	tatgtgacta	cgtaactttt	1500
78	gtctaccaca	acaaacatac	tctgtacaaa	aaagccaaaa	gtgaatttat	taaagagttg	1560
80	tcatattttg	caa					1573

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84 <211> LENGTH: 385
85 <212> TYPE: PRT
86 <213> ORGANISM: Drosophila melanogaster
88 <400> SEQUENCE: 2
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91 1 5 10 15
94 Glu Asp Asp Ser Thr Glu Val Asp Ile Lys Glu Asp Ile Pro Lys Thr
95 20 25 30
98 Val Glu Val Ser Gly Ser Glu Leu Thr Thr Glu Pro Met Ala Phe Leu
99 35 40 45
102 Gln Gly Leu Asn Ser Gly Asn Leu Met Gln Phe Ser Gln Gln Ser Val
103 50 55 60
106 Leu Arg Glu Met Met Leu Gln Asp Ile Gln Ile Gln Ala Asn Thr Leu
107 65 70 75 80
110 Pro Lys Leu Glu Asn His Asn Ile Gly Gly Tyr Cys Phe Ser Met Val
111 85 90 95
114 Leu Asp Glu Pro Pro Lys Ser Leu Trp Met Tyr Ser Ile Pro Leu Asn
115 100 105 110
118 Lys Leu Tyr Ile Arg Met Asn Lys Ala Phe Asn Val Asp Val Gln Phe
119 115 120 125
122 Lys Ser Lys Met Pro Ile Gln Pro Leu Asn Leu Arg Val Phe Leu Cys
123 130 135 140
126 Phe Ser Asn Asp Val Ser Ala Pro Val Val Arg Cys Gln Asn His Leu
127 145 150 155 160
130 Ser Val Glu Pro Leu Thr Ala Asn Asn Ala Lys Met Arg Glu Ser Leu
131 165 170 175
134 Leu Arg Ser Glu Asn Pro Asn Ser Val Tyr Cys Gly Asn Ala Gln Gly
135 180 185 190
138 Lys Gly Ile Ser Glu Arg Phe Ser Val Val Val Pro Leu Asn Met Ser
139 195 200 205
142 Arg Ser Val Thr Arg Ser Gly Leu Thr Arg Gln Thr Leu Ala Phe Lys
143 210 215 220
146 Phe Val Cys Gln Asn Ser Cys Ile Gly Arg Lys Glu Thr Ser Leu Val
147 225 230 235 240
150 Phe Cys Leu Glu Lys Ala Cys Gly Asp Ile Val Gly Gln His Val Ile
151 245 250 255
154 His Val Lys Ile Cys Thr Cys Pro Lys Arg Asp Arg Ile Gln Asp Glu
155 260 265 270
158 Arg Gln Leu Asn Ser Lys Lys Arg Lys Ser Val Pro Glu Ala Ala Glu
159 275 280 285
162 Glu Asp Glu Pro Ser Lys Val Arg Arg Cys Ile Ala Ile Lys Thr Glu
163 290 295 300
166 Asp Thr Glu Ser Asn Asp Ser Arg Asp Cys Asp Asp Ser Ala Ala Glu
167 305 310 315 320
170 Trp Asn Val Ser Arg Thr Pro Asp Gly Asp Tyr Arg Leu Ala Ile Thr
171 325 330 335
174 Cys Pro Asn Lys Glu Trp Leu Leu Gln Ser Ile Glu Gly Met Ile Lys
175 340 345 350

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178 Glu Ala Ala Ala Glu Val Leu Arg Asn Pro Asn Gln Glu Asn Leu Arg
179          355          360          365
182 Arg His Ala Asn Lys Leu Leu Ser Leu Lys Lys Arg Ala Tyr Glu Leu
183          370          375          380
186 Pro
187 385
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191 <211> LENGTH: 2600
192 <212> TYPE: DNA
193 <213> ORGANISM: Leptinotarsa decemlineata
195 <400> SEQUENCE: 3
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198 ttgtcttttc tttttctaatt tgtatcagaa tagctttttt aactgtgaaa accggaaggg      120
200 atgtctttctc agtcagactt tttacctcca gatgttcaaa atttcctctt ggcagaaatg      180
202 gaaggggaca atatggataa tctaaacttt ttcaaggacg aaccaacttt gaatgattta      240
204 aattattcaa acatcctaaa tggatcaata gttgctaatt atgattcaaa gatggttcatt      300
206 cttatttttc cgggagtaca aacaagtgtc ccatcaaatg atgaatacga tgggtccatat      360
208 gaatttgaag tagatgttca tcccactgtg gcaaaaaaatt cgtgggtgta ctctaccacc      420
210 ctgaataaag tttatatgac aatgggcagt ccatttcctg tagatttcag agtatcacat      480
212 cgacccccga acccattatt catcaggagc actcccgttt acagtgtctc ccaatttgct      540
214 caagaatgtg tttaccgggtg cctaaaccat gaattctctc ataaagagtc tgatggagat      600
216 ctcaaggaac acattcgccc tcatatcata agatgtgcca atcagtatgc tgcttactta      660
218 ggtgacaagt ctaaaaatga acgtctcagc gttgtcatac cattcggtat cccgcagacg      720
220 ggtactgaaa gtgttagaga aattttcgaa tttgtttgca aaaattcttg cccaagtcct      780
222 ggaatgaata gaagagctgt ggaaataata ttcacttttg aggataatca aggaactatc      840
224 tatggacgca aaacattaaa tgtgagaata tgctctgtgc caaaacgtga taaagagaaa      900
226 gatgaaaagg ataacactgc caacactaat ctgccgcatg gcaaaaagag aaaaatggag      960
228 aagccatcaa agaaacccat gcagacacag gcagaaaatg ataccaaaaga gtttactctg      1020
230 accataccgc tgggtgggtcg acataatgaa caaaatgtgt tgaagtattg ccatgatttg      1080
232 atggccgggg aaatcctgcg aaatatcggc aatggtactg aagggccgta caaaatagct      1140
234 ttaaacaaaa taaacacgtt gatacgtgaa agttccgagt gaccttatca attctatgta      1200
236 tatttcttat acaattccat tttcatattt ccatttgata ataagaaaca ttttagcacc      1260
238 ttttaatcct acactgcagg gaagtcaata tttctttagt tttttgcatg atattgtttg      1320
240 ttataacatt ttttttttca acaacagggtg acttgatttt tgtaagggtat ctcatatttt      1380
242 atgtttaaga cctaaaacac gaaacccaaa acatgaatgg tcattgaatt tggctcgata      1440
244 atcaatccaa tgttctttta agtaatatcg acctgttcac aacttttggt atgcactgaa      1500
246 tggcttttta ttattattat ttttcagcat tgtacatcat acttgcatag tttcagtttt      1560
248 aaatttttca aatgtttcat ttattttcat tcttacacct gaacttggat tttggacaca      1620
250 tggctttcac aatgttctat cacgaacagt atgataagcc aaagtaagag ttgataatag      1680
252 ttcataattaa tatctattgt aacaccgact attgttatat aaatagtcgt ttttttgta      1740
254 cttttcttgc tttattttat acacttgagt caagtgtagt cagtacattg actatgctgg      1800
256 aaaacctgtt ttgagtttat ttttacttac attcagttct catcattaga aattgtttat      1860
258 tttttgtgtg caatatttac gaaaaatggt gcaatactat aataggaaca ttaataaagt      1920
260 aacttgaaag catagagggtg gtgaattttg tttttgatca actttttgaa atttatgctc      1980
262 cattctataa gccagttttt tttgataaat tcaaaattca cgaataggta tcaacctgat      2040
264 tgcattgctta ttctatgttt gtcctaaaagc aggtctctat aaaacttctc taaaagttgt      2100
266 gcagagcaaa taacaaataa ttttttaatg gattatatca attcatgaac tggtttaatt      2160
268 gaaagagtag attattctat tgggttcaca aaaatataaa taatgtgtta ctatctggat      2220
270 catttgtttt tttttcattg agctatatatt tgtcattgta ttggtgaact ttccctaaat      2280

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272 cccagtgcc tagtcgacga tcggtctcgc tcccatccat caattattcg aaatctcatt 2340
274 tattttaag actgaggacg ggggtgggact gtcagtgtat ctgtttaatg agaaccatct 2400
276 tgtactagga ttgatatgtg aatctatgag taggtgcatt tttatatata tatctttatg 2460
278 tttatttagt attattgtac aggttatgta ctctagtggga agaatacata acctaattat 2520
280 tatatatgtt cgtaataata caaatttttt acgtttttta aatatatttt ctaaattattc 2580
282 aacaaaaaaaa aaaaaaaaaa 2600
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286 <211> LENGTH: 354
287 <212> TYPE: PRT
288 <213> ORGANISM: Leptinotarsa decemlineata
290 <400> SEQUENCE: 4
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296 Leu Ala Glu Met Glu Gly Asp Asn Met Asp Asn Leu Asn Phe Phe Lys
297 20 25 30
300 Asp Glu Pro Thr Leu Asn Asp Leu Asn Tyr Ser Asn Ile Leu Asn Gly
301 35 40 45
304 Ser Ile Val Ala Asn Asp Asp Ser Lys Met Val His Leu Ile Phe Pro
305 50 55 60
308 Gly Val Gln Thr Ser Val Pro Ser Asn Asp Glu Tyr Asp Gly Pro Tyr
309 65 70 75 80
312 Glu Phe Glu Val Asp Val His Pro Thr Val Ala Lys Asn Ser Trp Val
313 85 90 95
316 Tyr Ser Thr Thr Leu Asn Lys Val Tyr Met Thr Met Gly Ser Pro Phe
317 100 105 110
320 Pro Val Asp Phe Arg Val Ser His Arg Pro Pro Asn Pro Leu Phe Ile
321 115 120 125
324 Arg Ser Thr Pro Val Tyr Ser Ala Pro Gln Phe Ala Gln Glu Cys Val
325 130 135 140
328 Tyr Arg Cys Leu Asn His Glu Phe Ser His Lys Glu Ser Asp Gly Asp
329 145 150 155 160
332 Leu Lys Glu His Ile Arg Pro His Ile Ile Arg Cys Ala Asn Gln Tyr
333 165 170 175
336 Ala Ala Tyr Leu Gly Asp Lys Ser Lys Asn Glu Arg Leu Ser Val Val
337 180 185 190
340 Ile Pro Phe Gly Ile Pro Gln Thr Gly Thr Glu Ser Val Arg Glu Ile
341 195 200 205
344 Phe Glu Phe Val Cys Lys Asn Ser Cys Pro Ser Pro Gly Met Asn Arg
345 210 215 220
348 Arg Ala Val Glu Ile Ile Phe Thr Leu Glu Asp Asn Gln Gly Thr Ile
349 225 230 235 240
352 Tyr Gly Arg Lys Thr Leu Asn Val Arg Ile Cys Ser Cys Pro Lys Arg
353 245 250 255
356 Asp Lys Glu Lys Asp Glu Lys Asp Asn Thr Ala Asn Thr Asn Leu Pro
357 260 265 270
360 His Gly Lys Lys Arg Lys Met Glu Lys Pro Ser Lys Lys Pro Met Gln
361 275 280 285
364 Thr Gln Ala Glu Asn Asp Thr Lys Glu Phe Thr Leu Thr Ile Pro Leu
365 290 295 300

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368 Val Gly Arg His Asn Glu Gln Asn Val Leu Lys Tyr Cys His Asp Leu
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372 Met Ala Gly Glu Ile Leu Arg Asn Ile Gly Asn Gly Thr Glu Gly Pro
373                      325                      330                      335
376 Tyr Lys Ile Ala Leu Asn Lys Ile Asn Thr Leu Ile Arg Glu Ser Ser
377                      340                      345                      350
380 Glu Trp
384 <210> SEQ ID NO: 5
385 <211> LENGTH: 1291
386 <212> TYPE: DNA
387 <213> ORGANISM: Tribolium castaneum
389 <400> SEQUENCE: 5
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392 ttgattcaaa tcgtggattt ttattattta aatcatgagc caacaaagtc aatttttcgga      120
394 catcattcct gatgttgata aatttttggg agatcatgga ctcaaggacg atgtgggaag      180
396 aataatgcac gaaaacaacg tccatttagt aaatgacgac ggagaagaag aaaaatactc      240
398 taatgaagcc aattacactg aatcaatttt cccccccgac cagcccacaa acctaggcac      300
400 tgaggaatac ccaggccctt ttaattttct agtcctgatc agccccaacg agcaaaaatc      360
402 gccctgggag tattcggaaa aactgaacaa aatattcatc ggcatcaacg tgaaattccc      420
404 cgtggccttc tccgtgcaaa accgccccca gaacctgccc ctctacatcc gcgccacccc      480
406 cgtgttcagc caaacgcagc acttccaaga cctggtgcac cgctgcgtcg gccaccgcca      540
408 cccccaagac cagtccaaca aaggcgctcg cccccacatt ttccagcaca ttattagggtg      600
410 caccaacgac aacgccttat actttggcga taaaaacaca gggacgagac tcaacatcgt      660
412 cctgcctttg gccaccccc aggtggggga ggacgtggtc aaggagtttt tccagtttgt      720
414 gtgcaaaaac tcctgccctt tggggatgaa tcggcggccg attgatgtcg ttttcacct      780
416 ggaggataat aagggggagg ttttcgggag gaggttggtg ggggtgaggg tgtgttcgtg      840
418 tccgaagcgt gacaaggaca aggaggagaa ggacatggag agtgctgtgc ctccaaggag      900
420 gaagaagagg aagttgggga atgatgagcg aagggttgtg ccacagggga gctccgataa      960
422 taaaatattt gcgttaaata ttcattttcc tggcaagaag aattatttac aagccctcaa      1020
424 gatgtgtcaa gatatgctgg ctaatgaaat tttgaaaaaa caggaacaag gtggcgacga      1080
426 ttctgctgat aagaactgtt ataatgagat aactgttctc ttgaacggca cgccgcctt      1140
428 tgattagttt atttctatat ttaattttat actttgtact tatgcaatat tccagtttac      1200
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432 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a
435 <210> SEQ ID NO: 6
436 <211> LENGTH: 350
437 <212> TYPE: PRT
438 <213> ORGANISM: Tribolium castaneum
440 <400> SEQUENCE: 6
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446 Phe Leu Glu Asp His Gly Leu Lys Asp Asp Val Gly Arg Ile Met His
447                      20                      25                      30
450 Glu Asn Asn Val His Leu Val Asn Asp Asp Gly Glu Glu Glu Lys Tyr
451                      35                      40                      45
454 Ser Asn Glu Ala Asn Tyr Thr Glu Ser Ile Phe Pro Pro Asp Gln Pro
455                      50                      55                      60
458 Thr Asn Leu Gly Thr Glu Glu Tyr Pro Gly Pro Phe Asn Phe Ser Val
459 65                      70                      75                      80

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RAW SEQUENCE LISTING ERROR SUMMARY  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:31; Xaa Pos. 2  
Seq#:32; Xaa Pos. 2